

FIG. 1A

TCGATAGGTA	CCCACTATAG	GGCACGCGTG	GTCGACGGCC	CGGGCTGGTC	50
1					
TGGCAACTTC	AAGTGTGGGC	CTTTCAGACC	GGCATCATCA	GTGTTACGGG	100
51					
GAAGTCACTA	GGAATGCAGA	ATTGATTGAG	CACGGTGGCT	CACACCTGTA	150
101					
ATCCCAACAC	TCTGGGAGGC	CAAGGCAGGT	GGATCACTTG	TGGTCAGGAG	200
151					
TTTGAGACCA	GCCTGGCCAA	CATGGTGAAA	CCTCATCTCT	ACTAAAAATA	250
201					
CAAAAATTAG	CTGGGAATGG	TGGCACATGC	CTATAATCCC	AGTTACTCAG	300
251					
GAGGCTGAGG	CAGGAGAATC	ATTTGAACCT	GGGAGGCAGA	GGTTGCAGTG	350
301					
AGCCGAGATC	ACGCCACTGC	ACTCCAGCCT	GGGTGACACA	GCGAGACTCT	400
351					
GTCTCAAAAA	AAAAAAATG	CAGAATTTCA	GGCTTCACCC	CAGACCCACT	450
401					
GCATGACTGC	ATGAGAAGCT	GCATCTTAAC	AAGATCCCTG	GTAATTCATA	500
451					
CGCATATTAA	ATTTGGAGAT	GCACTGGCGT	AAGACCCTCC	TACTCTCTGC	550
501					
TTAGGCCCAT	GAGTTCTTCC	TTTACTGTCA	TTCTCCACTC	ACCCCAAAC	600
551					
TTGAGCCTAC	CCTTCCCACC	TTGGCGGTAA	GGACACAACC	TCCCTCACAT	650
601					
TCCTACCAGG	ACCCTAAGCT	TCCCTGGGAC	TGAGGAAGAT	AGAATAGTTC	700
651					
GTGGAGCAAA	CAGATATACA	GCAACAGTCT	CTGTACAGCT	CTCAGGCTTC	750
701					

T01E0-00271360



FIG. 1B

751 801 851 901 951 1001 1051 1101 1151 1201 1251 1301 1351 1401 1451

TGGAAGTTCT ACAGCCTCTC CCGACAAAGT ATTCCACTTT CCACAAGTAA 800
 CTCTATGTGT CTGAGTCTCA GTTCCACTT TTCTCTCTCT CTCTCTCTCT 850
 CAACTTTCTG AGACAGAGTT TCACTTAGTC GCCCAGGCTG GAGTGCAGGG 900
 GCACAATCTC GGCTCACTGC AACCTCCACC TCCTGGGTTC AAGTGTCTTCT 950
 CCTGTCTCAG CCTCCCAGT AGCTGGGATT ACAGGCACAC ACCACCGCGT 1000
 TAGTTTTTGT ATTTTGGTA GAGATGGTGT TTCGCCATAT TGGCCAGGCT 1050
 GATCTCGAAC TCCTGACCTC AGGTGATCCG CCCACCTCGG CCTCCCAAAG 1100
 TGCTGGGATT ACAGGCATGA GCCACCACGC CCGGCTGATC TCTTTTCTAT 1150
 TTAAATAGAG ATCAAACCTCT CTGTGTTGCC TAGGCTGGTC TTGAACCTCT 1200
 GGCTCGAGT GATCCTCCCA CCTTGGCCTC CCAAAGTGT GAGATTACAG 1250
 GCATGAGCCA CTGTGCCTGG CCTCAGTTCT ACTACAAAAG GAAGCCAGTA 1300
 CCAGCTACCA CCCAGGGTGG CTGTAGGGCT ACAATGGAGC ACACAGAACC 1350
 CCTACCCAGG GCCCGGAAGA AGCCCCGACT CCTCTCCCCT CCCTCTGCCC 1400
 AGAACTCCTC CGCTTCTTTC TGATGTAGCC CAGGGCCGGA GGAGGCAGTC 1450
 AGGGAAGTTC TGTCTCTTTT TCATGTTATC TTACGAGGTC TCTTTTCTCC 1500

ATTCTCAGTC 1501	CAACAAATGG	TTGCTGCCCA	AGGCTGACTG	TGCCCCACCC	1550
CAACCCCTGC 1551	TGGCCAGGGT	CAATGTCTGT	CTCTCTGGTC	TCTCCAGAAG	1600
TCTTCCATGG 1601	CCACCTTCGT	CCCCACCCTC	CAGAGGAATC	TGAAACCGCA	1650
TGTGCTCCCT 1651	GGCCCCCACA	GCCCCTGCTT	CTCCCAGAGC	AGCAGTACCT	1700
AAGCCTCAGT 1701	GCACTCCAAG	AATTGAAACC	CTCAGTCTGC	TGCCCCCTCC	1750
CACCAGAATG 1751	TTTCTCTCCC	ATTCTTACCC	ACTCAAGGCC	CTTTCAGTAG	1800
CCCCTTGAG 1801	TATTCTCTTC	CTACATATCA	GGGCAACTTC	CAAACCTATC	1850
ACCCTTCTGA 1851	GGGGTGGGGG	AAAGACCCCC	ACCACATCGG	GGGAGCAGTC	1900
CTCCAAGGAC 1901	TGGCCAGTCT	CCAGATGCCC	GTGCACACAG	GAACACTGCC	1950
TTATGCACGG 1951	GAGTCCCAGA	AGAAGGGGTG	ATTTCTTTCC	CCACCTTAGT	2000
TACACCATCA 2001	AGACCCAGCC	AGGGCATCCC	CCCTCCTGGC	CTGAGGGCCA	2050
GCTCCCCATC 2051	CTGAAAAACC	TGTCTGCTCT	CCCCACCCCT	TTGAGGCTAT	2100
AGGGCCCAAG 2101	GGGCAGGTTG	GACTGGATTG	CCCTCCAGCC	CCTCCCGCCC	2150
CCAGGACAAA 2151	ATCAGCCACC	CCAGGGGCAG	GGCCTCACTT	GCCTCAGGAA	2200
CCCCAGCCTG 2201	CCAGCACCTA	TTCCACCTCC	CAGCCCAGCA		2239



[illegible]

FIG. 2B

CCCAGAGAAAGGTCCTAGTGGAAGTGGGGGCCACTGAAGGGCTGATGG 900
 851
 GGTTCTGTCCTTTCCCCCATGCTGGGTGGACTTAAAGTCTGCGATGTGTG 950
 900
 TAGGGGGTAGAAGACAACAGAACCTGGGGGCTCCGGCTGGGAGCAGGAGG 1000
 951
 AACTCTCACCAGACGATCTCCAAATTTACTGTGCAATGGACGATCAGGAA 1050
 1001
 ACTGGTTCAGATGTAGCTTCTGATACAGTGGGTCTGAGGTAAAACCCGAA 1100
 1051
 ACTTAATTTCTTTCAAAAATTTAAAGTTGCATTTATTATTTTATATGTGT 1150
 1101
 GCCCATATGTGTGCCACAGTGTCTATGTGGAGGTCAGAGGGCAAGTTGTG 1200
 1151
 GGCATTGGCTCTCTCCTTTTATAATGTGGCTTCTGGGGACCAAATGTCA 1250
 1201
 GGCATGGTGGCAAGAGCTTTTACCTGTTGAGCCATCTCATGGTTTCGTAA 1300
 1251
 AACTTCCTATGACGCTTACAGGTAACGCAGAGACACAGACTCACATTTGG 1350
 1301
 AGTTAGCAGATGCTGTATTGGTGTAACACTCATAACAGACACACACAC 1400
 1351
 ATACTCATAACACACACACACTTATCATGACACACATACTCGTA 1450
 1401
 TACACACAGACACACACATGCACTCTCACATTACATATTCATACACA 1500
 1451
 TCCACACACACTCATCCACACACAGACACACATACTCATCCACACA 1550
 1501
 CACACACACATACTCATAACACACACAGACACACATACTCATAACA 1600
 1551
 CACACAGACACACATATAATCATAACACAGACACACTCATAATG 1650
 1601
 TGCACACACACTCATCCACACACACACTCATAACACACACACTCA 1700
 1651

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FIG: 2C

TACACACACACTCATACACACACACGAGGTTTTCTCAGGCTGCCT
1701 1750

TTGGGTGGAGACTGGAAGTCTGTTTTTCAGCTCCTTGGCTTTTTG
1751 1800

TCCCTTTAGATGAGATCTCCTCCTCACTTTACACACAGAAAGATCACACA
1801 1850

CGAGGGAGAACTGGCGGTGCGGAAGAGGGCTACACGGTAGGGTGTGAGG
1851 1900

TCAGGAGATCTTCTGGCAAGTCTCAAACCTCCACATAGCACAGTGTTTA
1901 1950

CGTGAGGATTTAGGAGGAATCAGGAAGAGGATTGGTTTACTGCAGAGCAG
1951 2000

ACCATATAGGTCCACTCCTAAGCCCCATTTGAAATTAGAAGTGAGACAGT
2001 2050

GTGGGATAAAAAGAGCAGATCTCTGGTCACATTTTTAAAGGGATATGAGG
2051 3000

GTCCTGTGCCTTTAAGCCTTCCCATCTCCCTCCAATCCCCCCTCACCTTC
2101 2150

CCCACCCTAACCTCCCCAGGTTTCTGGAGGAGCAGAGTTGCGTCTTCTC
2151 2200

CCTGCCCTGCCGAGCTGCTCACTGGCTGCTCTAGAGGCTGTGCTTTGCGG
2201 2250

TCTCCATGGAAACCATTAGTTGCTAAGCAACTGGAGCATCATCTGTGCTG
2251 2300

AGCTCAGGTCCTATCGAGTTCACCTAGCTGAGACACCCACGCCCCCTGCAG
2301 2350

CCACTTTGCAGTGACAAGCCTGAGTCTCAGGTTCTGCATCTATAAAAACG
2351 2400

AGTAGCCTTTTCAAGAGGGCATGCAGAGCCCCCTGGCCAGCGTCTAGAGGA
2401 2450

GAGGTGACTGAGTGGGGCCATGTCACTCGTCCATGGCTGGAGAACCTCCA
2451 2500

TCAGTCTCCCAGTTAGCCTGGGGCAGGAGAGAACCAGAGGAGCTGTGGCT
2501 2550

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TOTED-26271860

FIG. 2D

GCTGATTGGATGATTACGTACCCAATCTGTTGTCCAGGCATCGAACCC
 2551 2600
 CAGAGCGACCTGCACACATGCCACCGCTGCCCCGCCCTCCACCTCCTCTG
 2601 2650
 CTCCTGGTTACAGGATTGTTTTGTCTGAAGGGTTTTGTTGTGCTACTT
 2651 2700
 TTTGCTTTGTTTTTTCTTTTTTAACATAAGGTTTCTCTGTGTAGCCCTAG
 2701 2750
 CTGTCTGGAACTCACTCTGTAGACCAGGCTGGCCTCAAACCTCAGAAATC
 2751 2800
 CACCTTCCTCCCAAGTGCTGGGATTAAAGGCATTGCGACCATCGCCCAGC
 2801 2850
 CCCCAGTCTTGTTTCCTAAGGTTTTCTGCTTTACTCGCTACCCGTTGCA
 2851 2900
 CAACCGCTTGCTGTCCAAGTCTGTTTGTATCTACTCCACCGCCCACTAGC
 2901 2950
 CTTGCTGGACTGGACCTACGTTTACCTGGAAGCCTTCACTAACTTCCCTT
 2951 3000
 GTCTCCACCTTCTGGAGAAATCTGAAGGCTCACACTGATACCCTCCGCTT
 3001 3050
 CTCCCAGAGTCGCAGTTTCTTAGGCCTCAGTTAAATACCAGAATTGGATC
 3051 3100
 TCAGGCTCTGCTATCCCCACCCTACCTAACCAACCCCCTCCTCTCCCATC
 3101 3150
 CTTACTAGCCAAAGCCCTTTCAACCCTTGGGGCTTTTCTACACCTACAC
 3151 3200
 ACCAGGGCAATTTTAGAACTCATGGCTCTCCTAGAAAACGCCTACCTCCT
 3201 3250
 TGGAGACTGACCCTCTACAGTCCAGGAGGCAGACACTCAGACAGAGGAAC
 3251 3300
 TCTGTCCTTCAGTCGCGGGAGTTCCAGAAAGAGCCATACTCCCCTGCAGA
 3301 3350
 GCTAACTAAGCTGCCAGGACCCAGCCAGAGCATCCCCCTTTAGCCGAGGG
 3351 3400

2025-02-24 10:00

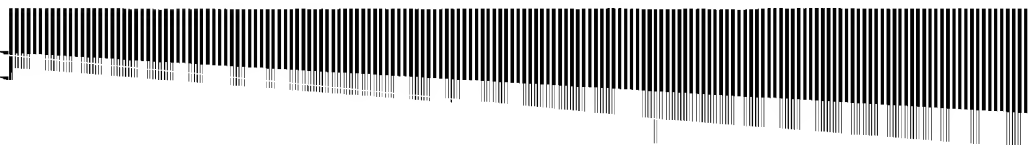


FIG. 2E

CCAGCTCCCAGAATGAAAAACCTGTCTGGGGCCCCTCCCTGAGGCTACA 3450

3401
GTCGCCAAGGGGCAAGTTGGACTGGATTCCCAGCAGCCCCTCCCACTCCG 3500

3451
AGACAAAATCAGCTACCCTGGGGCAGGCCTCATTGGCCCCAGGAAACCCC 3550

3501
AGCCTGTCAGCACCTGTTCCAGGATCCAGTCCCAGCGCAGTA 3592

3592 3592 3592

Figure 3A

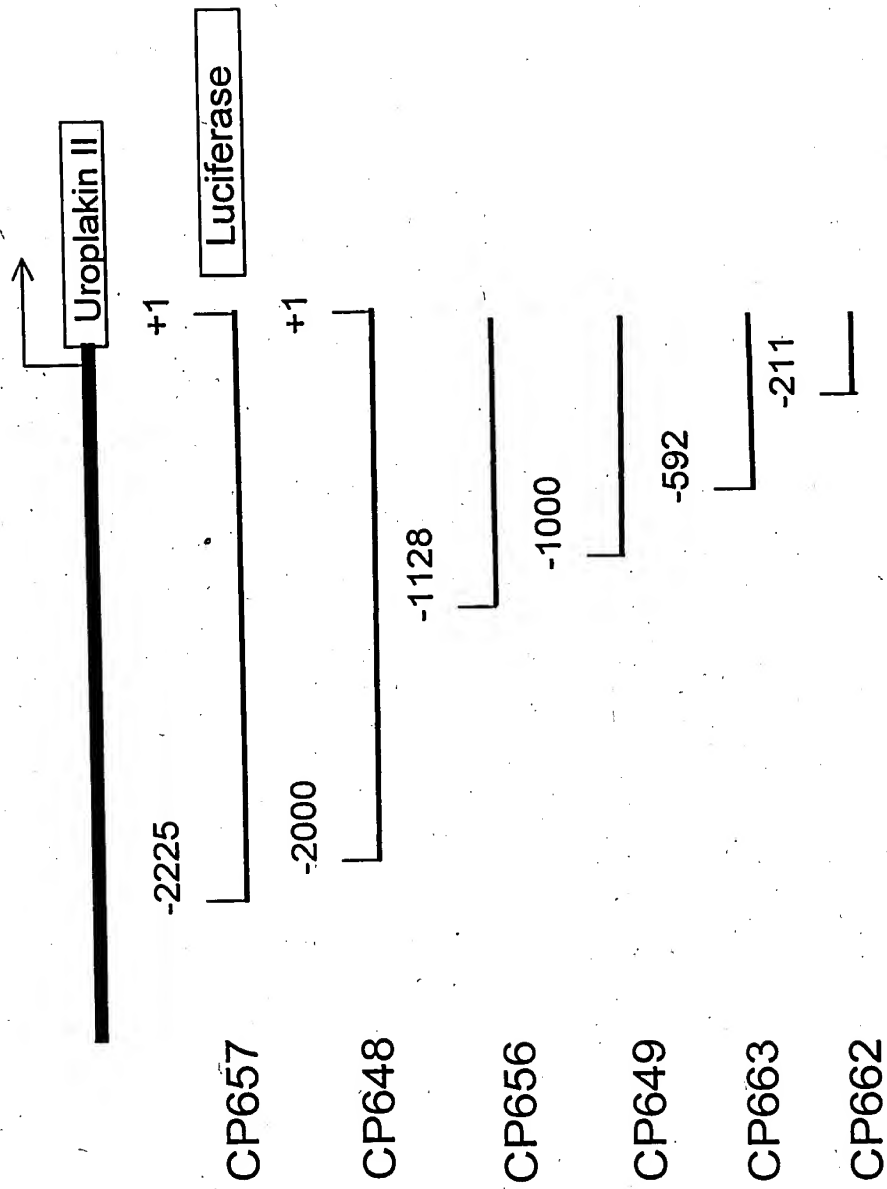


Figure 3B

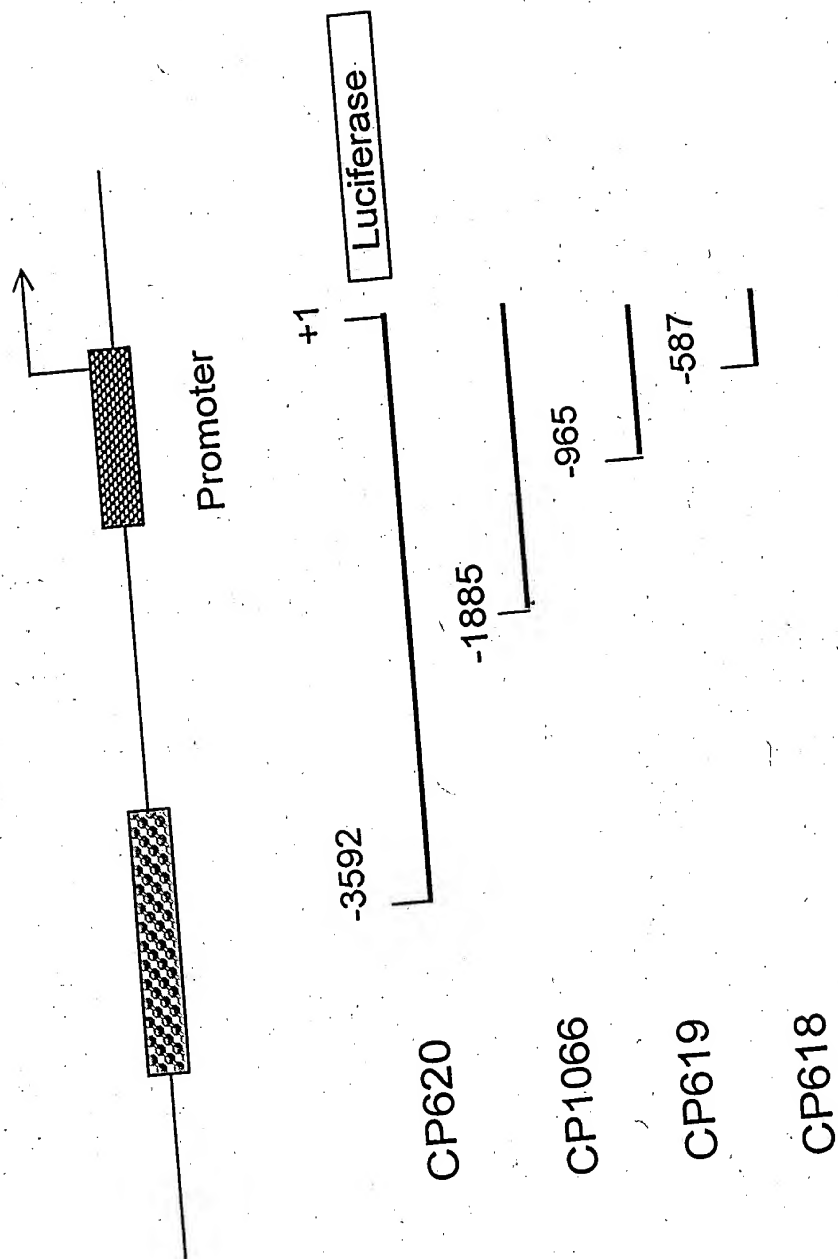


Figure 4A

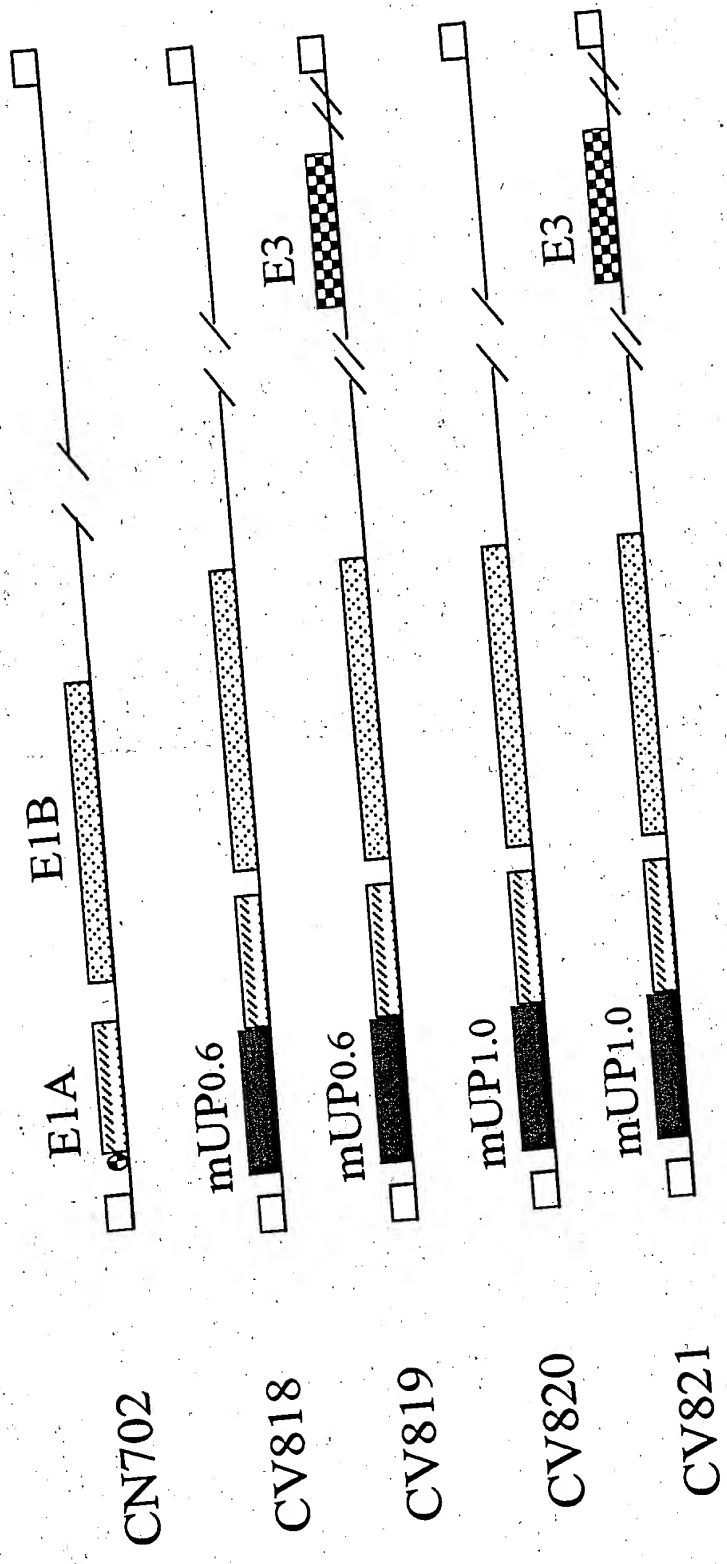


Figure 4B

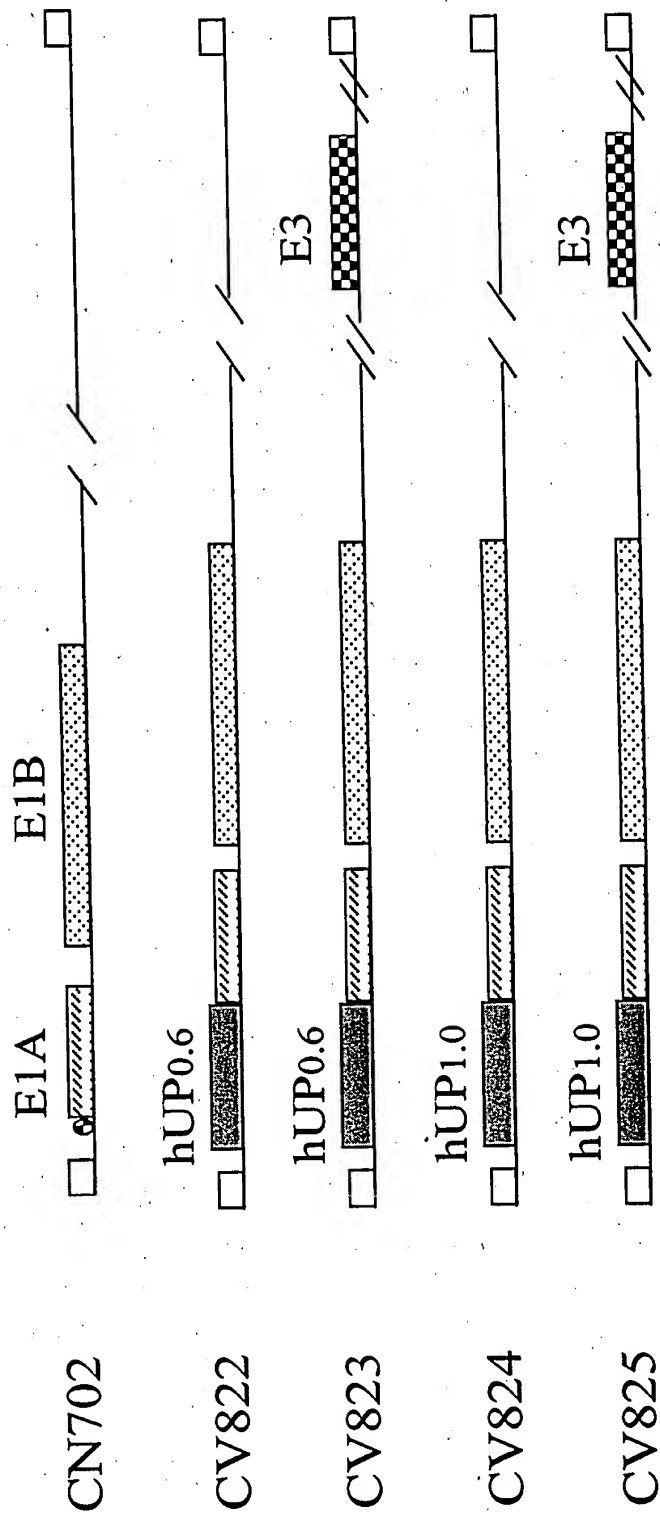


Figure 4C

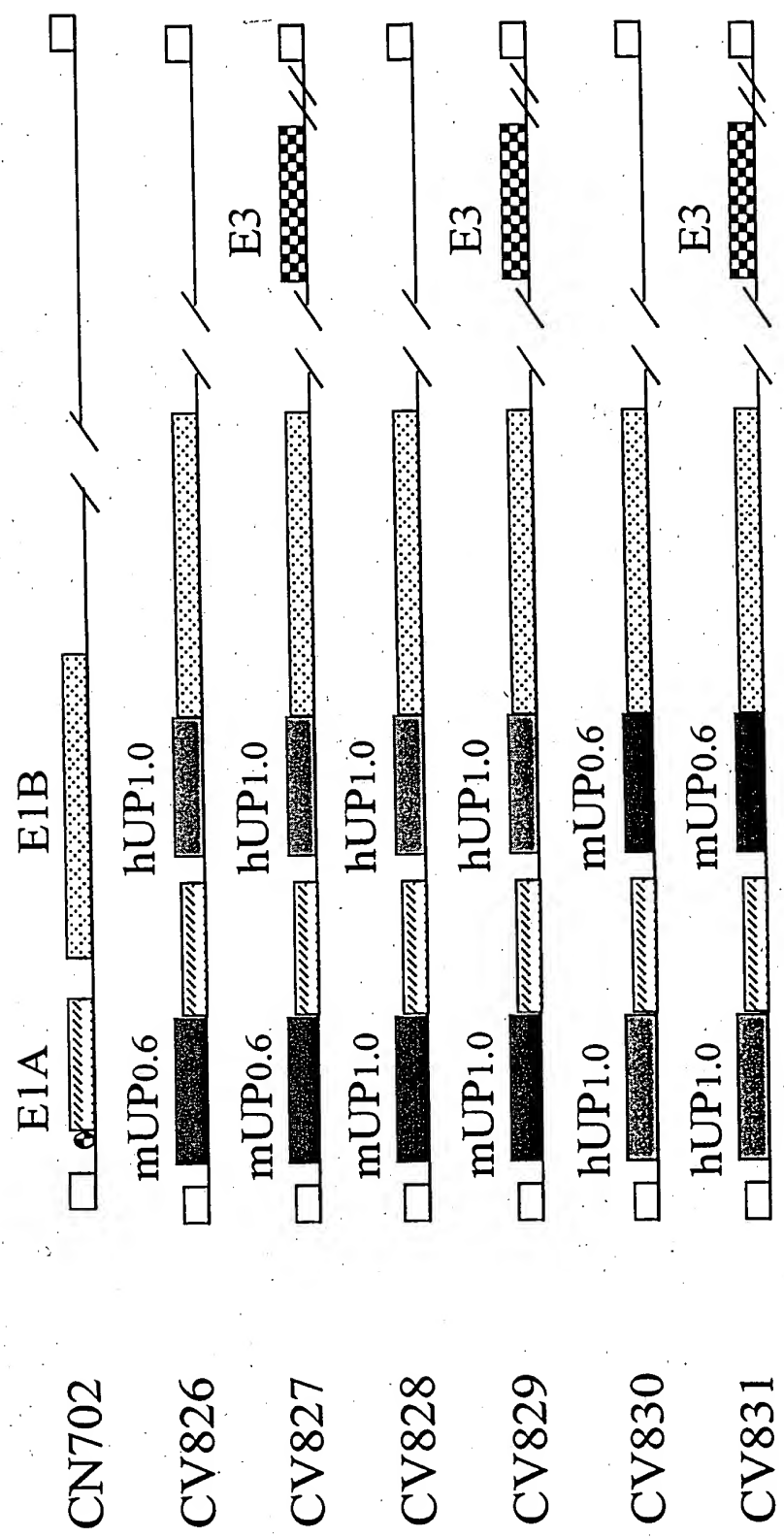
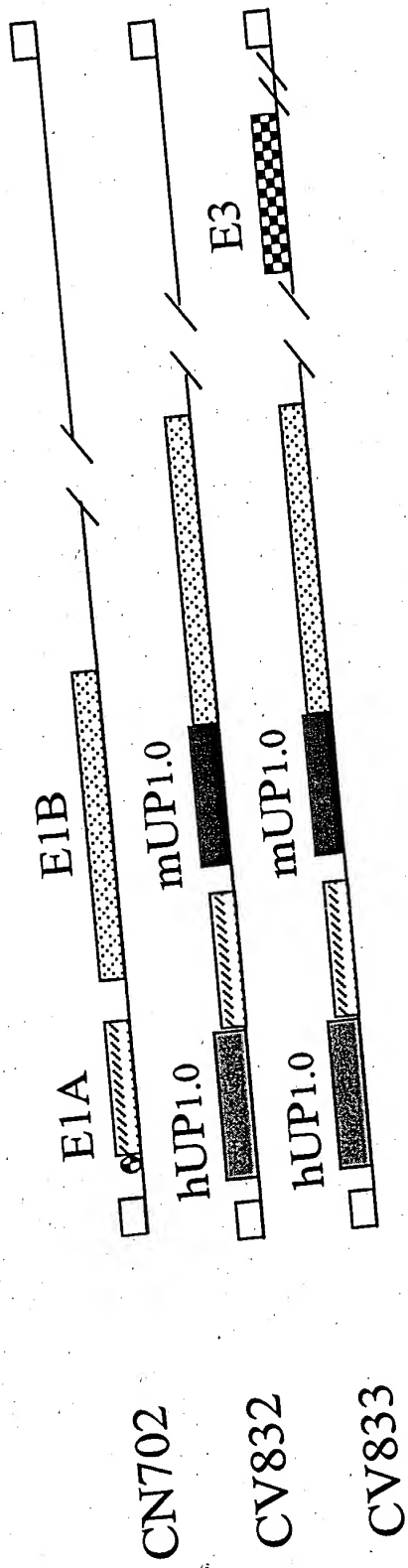


Figure 4D



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Figure 4E

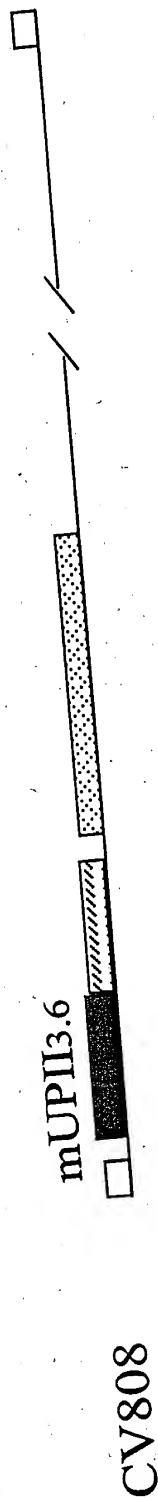
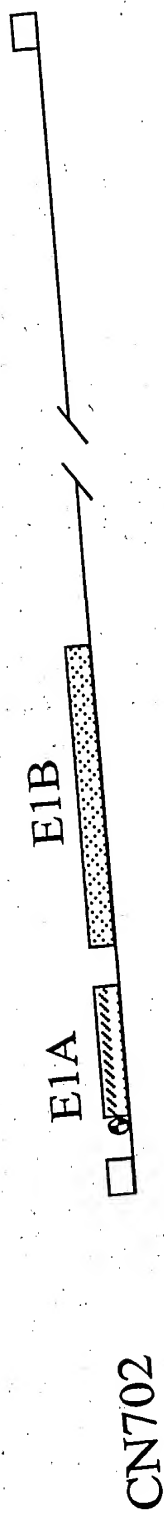


Figure 4F

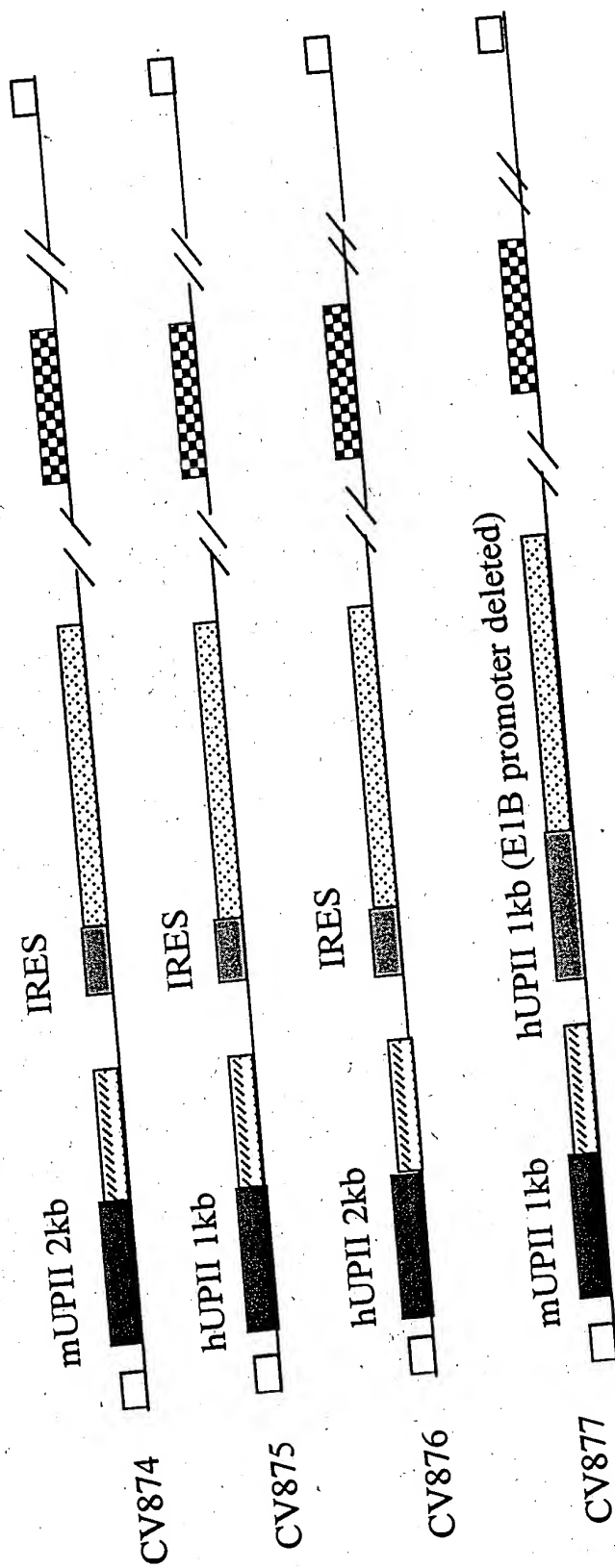
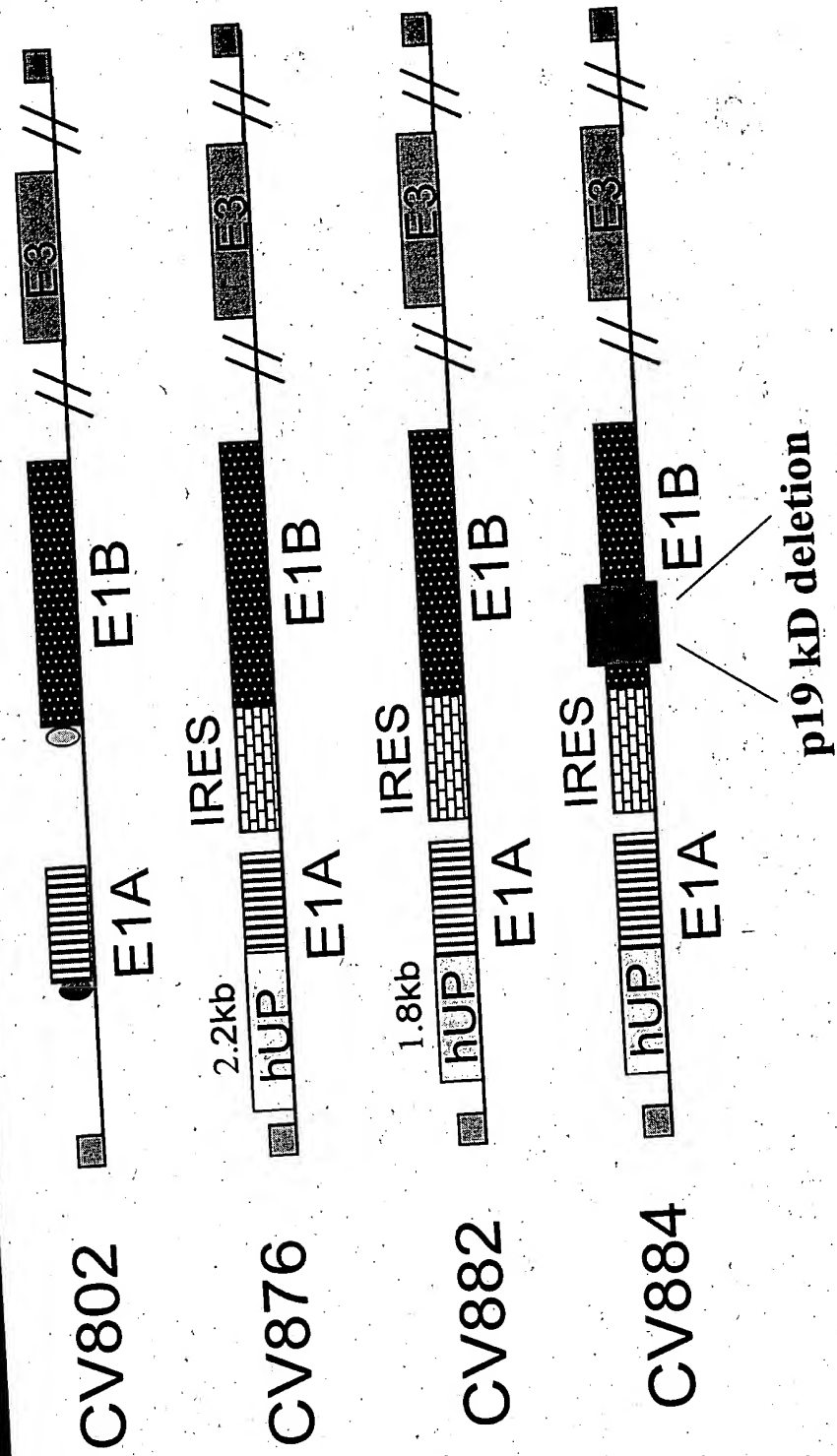


Figure 4G

Structure of CV876, CV882 and CV884



Bladder Specificity

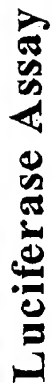


FIG. 7

FIG. 7

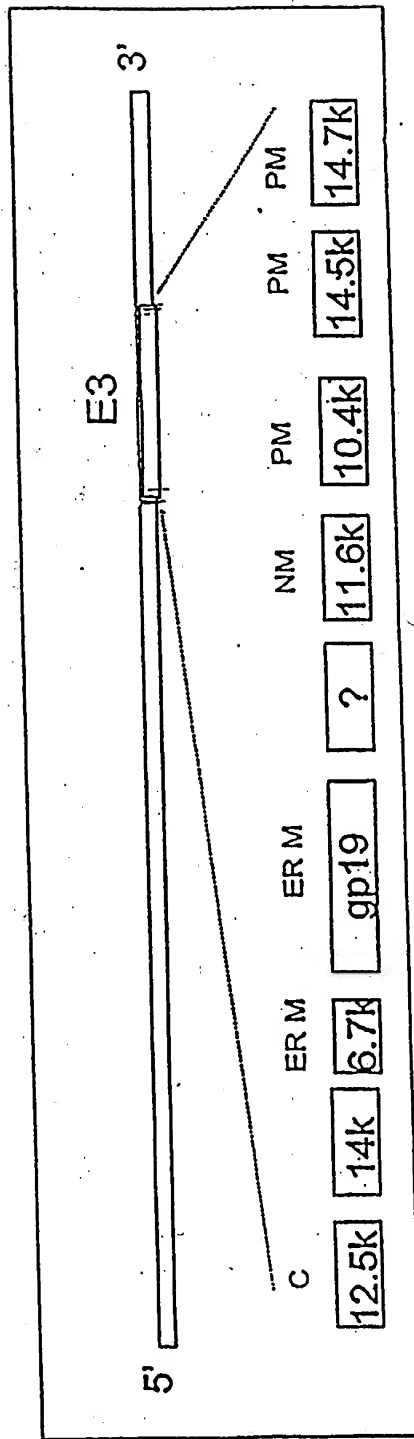


FIG. 8

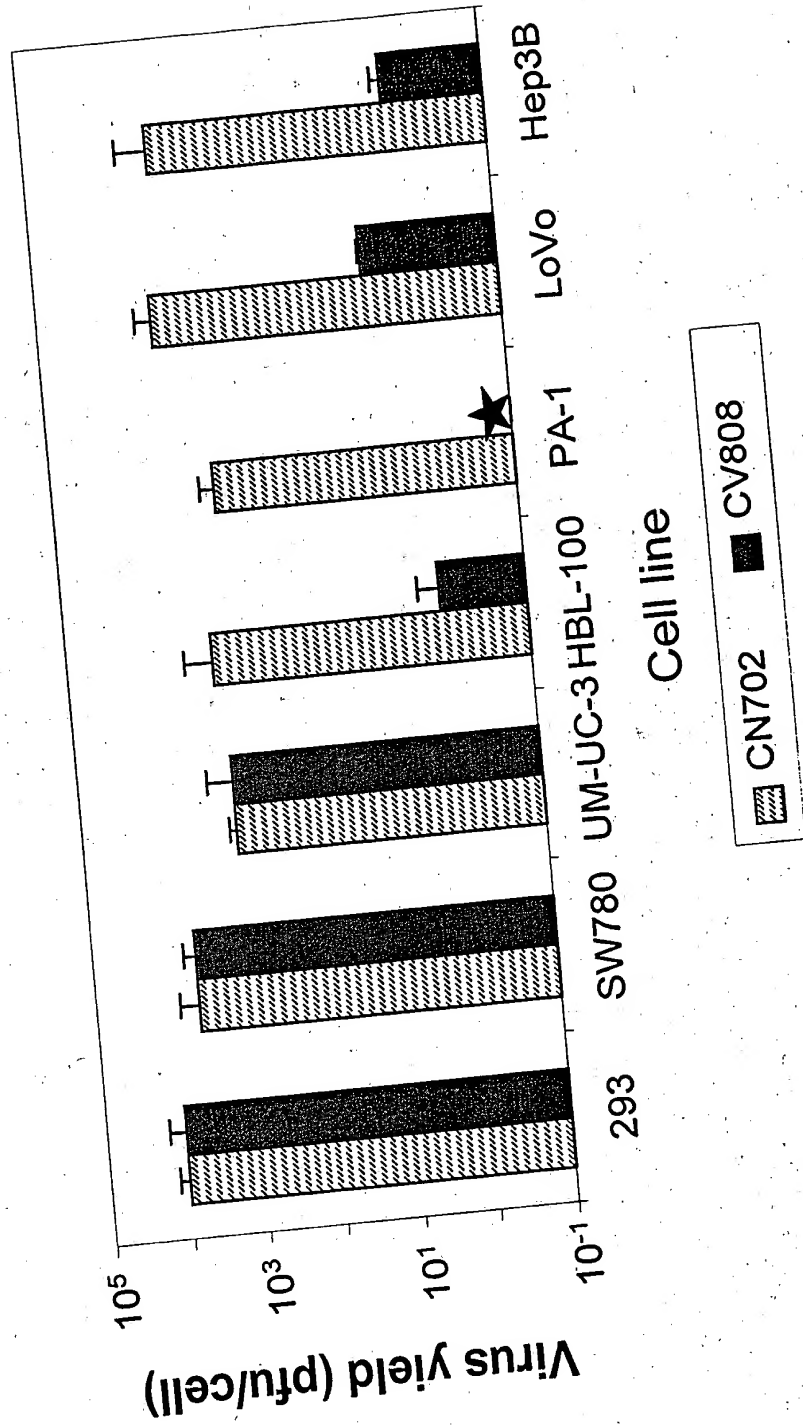


FIG. 9

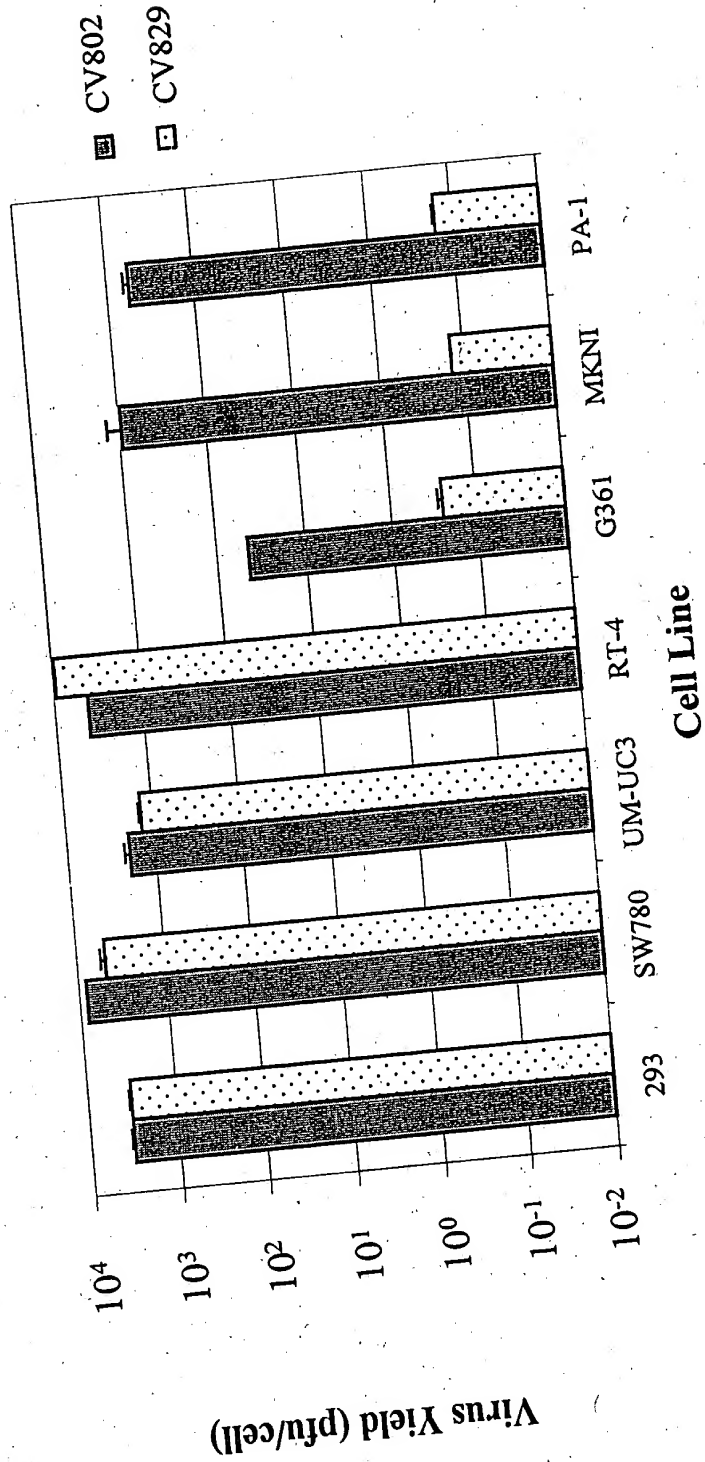
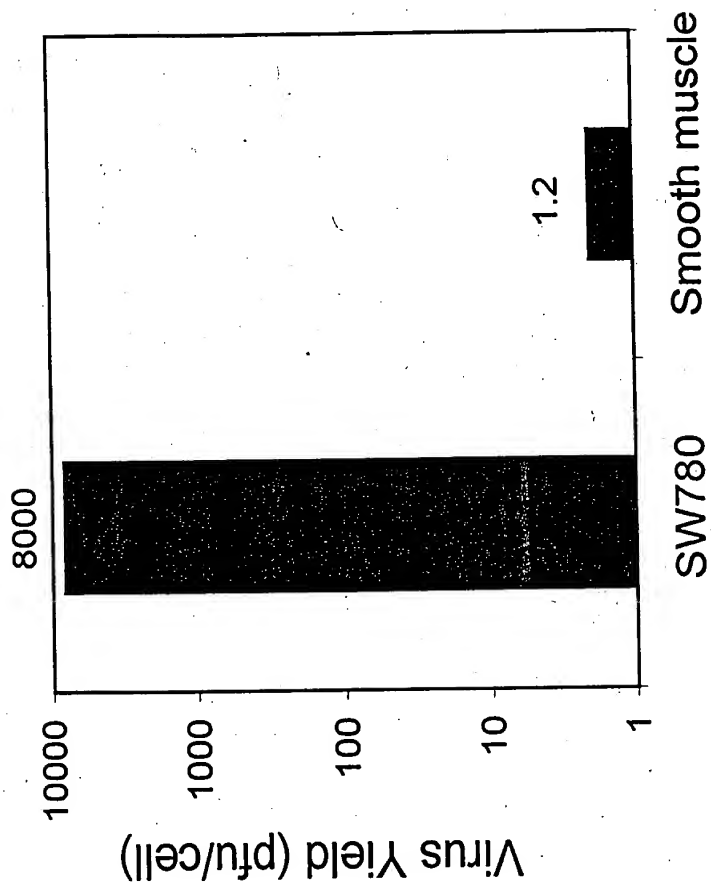
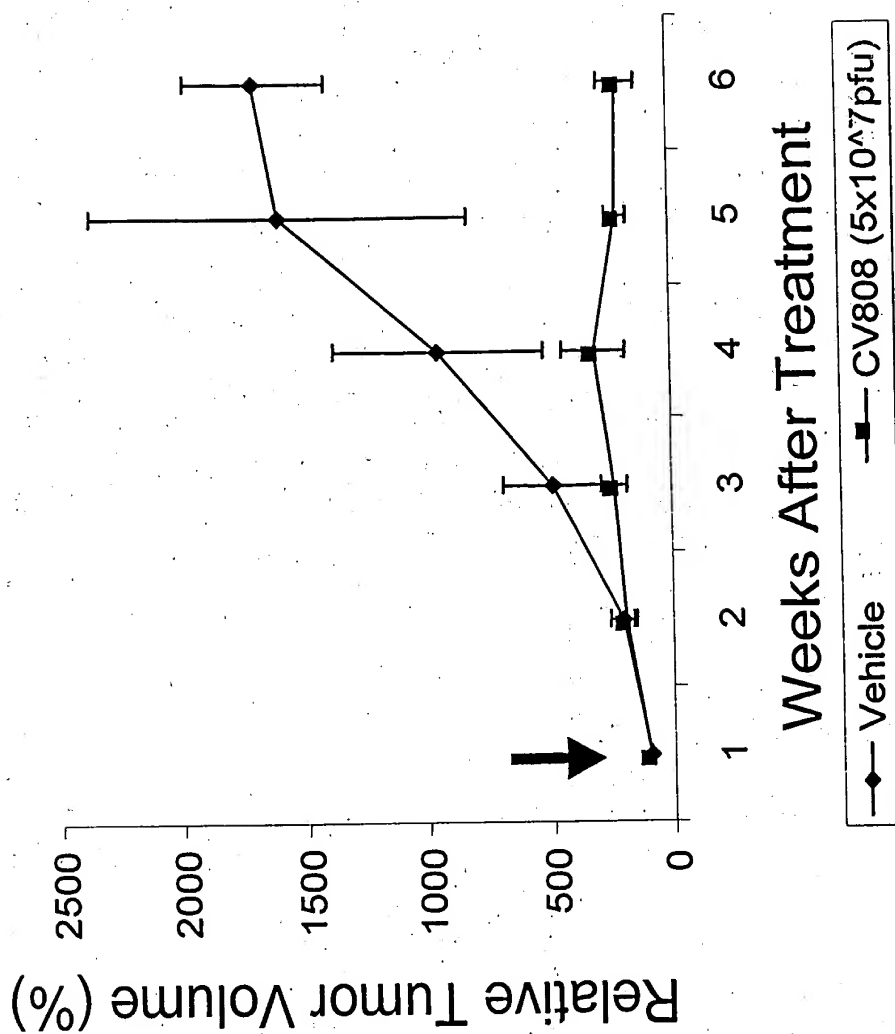


FIG. 10



TOP SECRET

FIG. 11



[illegible]

Met. Thr Gly Ser Thr Ile Ala Pro. Thr Thr Asp Tyr Arg Asn Thr
1 5 10 15

Thr Ala Thr Gly Leu Thr Ser Ala Leu Asn Leu Pro Gln Val His Ala
20 25 30

CTT ATG TTT GTT TGC CTT ATT ATT ATG TGG CTT ATT TGT TGC CTA AAG
190
Leu Met Phe Val Cys Leu Ile Ile Met Trp Leu Ile Cys Cys Leu Lys
50 55 60

CCA CAC AAT GAA AAA ATT CAT AGA TTG GAC GGT CTG AAA CCA TGT TCT
286
Pro His Asn Glu Lys Ile His Arg Leu Asp Gly Leu Lys Pro Cys Ser
80 85 90 95

CTT CTT TTA CAG TAT GAT TAA
307
Leu Leu Leu Gln Tyr Asp
100

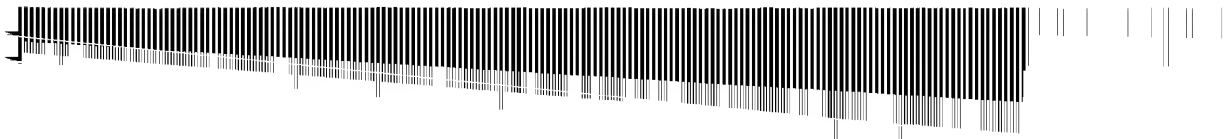


FIG. 13

Region E3 of Adenovirus

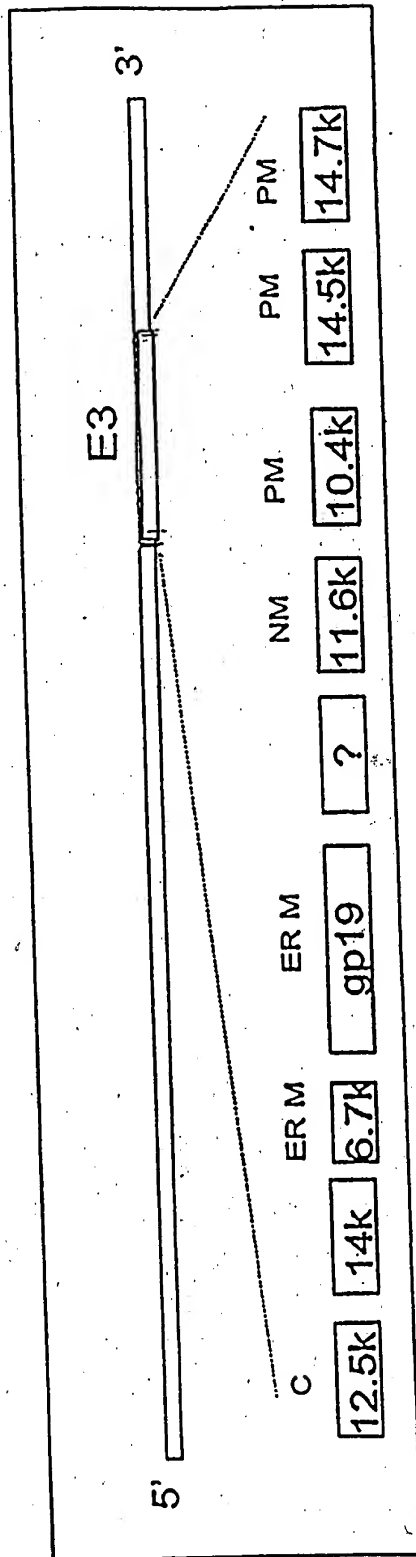


FIG. 14

Virus Yield of CV884

